# APPENDIX

Elected Claims:

89. A method comprising steps of:

providing a collection of mutant allergen genes that differ in sequence from a gene encoding a naturally-occurring allergen protein in that each of the mutant allergen genes contains one or more nucleotide deletion, addition, or substitution as compared with the gene encoding the naturally-occurring allergen protein;

expressing a collection of mutant allergen proteins from the collection of mutant allergen genes;

screening the collection of mutant allergen proteins to identify at least one mutant allergen protein whose affinity for anti-allergen IgE is reduced as compared with that of the naturally-occurring allergen protein; and

screening the collection of mutant allergen proteins to identify those that retain at least one desired biological activity,

so that mutant allergen proteins that have reduced IgE binding and yet retain the at least one desired biological activity are identified.

90. The method of claim 89, wherein the at least one desired biological activity is selected from the group consisting of T cell stimulatory activity; IgG binding activity; and ability, when administered to an individual sensitive to the naturally-occurring allergen protein, to promote desensitization of the individual to the naturally-occurring allergen protein.

91. The method of claim 89, wherein the naturally-occurring allergen protein contains at least one conformational epitope.

92. The method of claim 89, wherein the step of providing a collection of mutant allergen genes comprises providing at least one mutant allergen gene that contains a mutation disrupting a conformational epitope.

93. The method of claim 89, wherein the step of providing comprises:

providing the gene encoding the naturally-occurring allergen protein; and

exposing the gene to mutagenesis conditions so that mutations are introduced randomly within the gene sequence and the collection of mutant allergen genes is produced, which collection is characterized by a random distribution of sequence alterations as compared with the gene encoding the naturally-occurring allergen protein.

94. The method of claim 89, wherein the step of screening the collection of mutant allergen proteins to identify at least one mutant allergen protein whose affinity for anti-allergen IgE is reduced as compared with that of the naturally-occurring allergen protein comprises:

providing a collection of IgEs or Fabs representing those expressed in an individual who is allergic to the naturally-occurring allergen protein; and

detecting binding of IgEs or Fabs from the collection to mutant allergen polypeptides as compared with naturally-occurring allergen protein.

95. The method of claim 94, wherein the individual who is allergic to the naturally-occurring allergen protein is a human individual.

96. The method of claim 89, 94, or 95wherein the naturally-occurring allergen protein comprises a polypeptide that is naturally found in a source selected from the group consisting of insects, foods, molds, dusts, pollens, plants, fish, shellfish, and mammals.

97. The method of claim 95, wherein the naturally-occuring allergen protein comprises a polypeptide that is naturally found in a food.

Withdrawn Claims:

98. A method comprising steps of:

providing a collection of mutant genes that differ in sequence from a gene encoding a therapeutic polypeptide whose therapeutic activity is reduced by IgG binding in that each of the mutant genes contains one or more nucleotide deletion, addition, or substitution as compared with the gene encoding the therapeutic polypeptide;

expressing a collection of mutant proteins from the collection of mutant genes;

screening the collection of mutant proteins to identify at least one mutant protein whose affinity for anti-therapeutic-polypeptide IgG is reduced as compared with that of the original therapeutic polypeptide; and

screening the collection of mutant proteins to identify those that retain therapeutic activity,

so that mutant proteins that have reduced IgG binding and yet retain therapeutic activity are identified.

99. The method of claim 98, wherein the step of providing comprises:

providing the gene encoding the therapeutic polypeptide; and

exposing the gene to mutagenesis conditions so that mutations are introduced randomly within the gene sequence and the collection of mutant genes is produced, which collection is characterized by a random distribution of sequence alterations as compared with the gene encoding the therapeutic polypeptide.

100. The method of claim 98, wherein the step of screening the collection of mutant proteins to identify at least one mutant protein whose affinity for anti-therapeutic-polypeptide IgG is reduced comprises:

providing a collection of IgGs or Fabs representing those expressed in an individual in whom the therapeutic activity of the therapeutic protein is reduced by IgG binding; and

detecting binding of IgGs or Fabs from the collection to mutant proteins as compared with the therapeutically active protein.

101. The method of claim 95, wherein the therapeutic polypeptide is selected from the group consisting of GM-CSF and streptokinase.

102. The method of claim 100, wherein the therapeutic polypeptide is streptokinase and the therapeutic activity comprises an ability to disrupt blot clots.

103. The method of claim 100, wherein the therapeutic polypeptide is GM-CSF, and the therapeutic activity comprises trophic activity.

104. A method comprising steps of:

providing a collection of mutant genes that differ in sequence from a gene encoding a protein expressed by a therapeutic virus whose therapeutic activity is reduced by clearing, the mutant genes differing from the viral gene in that each mutant gene contains one or more nucleotide deletion, addition, or substitution as compared with the viral gene;

expressing a collection of mutant proteins from the collection of mutant genes;

screening the collection of mutant proteins to identify at least one mutant protein whose ability to activate T cells is reduced compared with that of the viral protein; and

screening the collection of mutant proteins to identify those that successfully participate in a biological activity selected from the group consisting of viral infection, viral capsid assembly, and cell entry by virus expressing mutant protein,

so that mutant proteins that have reduced T cell stimulatory activity yet retain activity within the virus are identified.

105. The method of claim 104, wherein the step of providing comprises:

providing the gene encoding the viral protein; and

exposing the gene to mutagenesis conditions so that mutations are introduced randomly within the gene sequence and the collection of mutant genes is produced, which collection is characterized by a random distribution of sequence alterations as compared with the gene encoding the viral protein.